

10/534744

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/534744
Source: PCT
Date Processed by STIC: 5/20/5

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 05/20/2005

PATENT APPLICATION: US/10/534,744

TIME: 12:17:24

Input Set : A:\47968-A Sequence Listing.txt

Output Set: N:\CRF4\05202005\J534744.raw

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3 <110> APPLICANT: University of Saskatchewan Technologies Inc.
5 <120> TITLE OF INVENTION: PLANT STRESS TOLERANCE GENES, AND USES THEREFOR
7 <130> FILE REFERENCE: 47968-PT
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/534,744
C--> 9 <141> CURRENT FILING DATE: 2005-05-12
9 <150> PRIOR APPLICATION NUMBER: US 60/426,012
10 <151> PRIOR FILING DATE: 2002-10-14
12 <160> NUMBER OF SEQ ID NOS: 4
14 <170> SOFTWARE: PatentIn version 3.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 1420
18 <212> TYPE: DNA
19 <213> ORGANISM: Bromus
21 <220> FEATURE:
22 <221> NAME/KEY: misc_feature
23 <222> LOCATION: (1212)..(1212)
24 <223> OTHER INFORMATION: n = a, c, g, or t
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (77)..(1231)
30 <223> OTHER INFORMATION:
W--> 32 <400> 1
33 gtcgcaatcc attcagagca cgcaaagcac gcgagcagct gcgcatctcta gattctagct 60
35 cgggacgatac agatca atg gcg gtc atg tcg cgg tcc agg agg ctg gcg gcg 112
36 Met Ala Val Met Ser Arg Ser Arg Leu Ala Ala
37 1 5 10
39 ccc gcg ctg ctg gtg ctg cta gcg ctg gcg gcc gtg gcc gtg gcg gag 160
40 Pro Ala Leu Leu Val Leu Leu Ala Leu Ala Ala Val Ala Val Ala Glu
41 15 20 25
43 acg acg ctg gac ggc gcg gag gtg gcg ccg ggc aag gag gag tcg tcg 208
44 Thr Thr Leu Asp Gly Ala Glu Val Ala Pro Gly Lys Glu Glu Ser Ser
45 30 35 40
47 tgg gcg ggg tgg gcc aag gac aag gtc tcg gaa ggc ctc ggc ctg gac 256
48 Trp Ala Gly Trp Ala Lys Asp Lys Val Ser Glu Gly Leu Gly Leu Asp
49 45 50 55 60
51 aag atc tcc gag ggg ctc ggg ctc aag cac cac gcc gac gag gag gag 304
52 Lys Ile Ser Glu Gly Leu Gly Leu Lys His His Ala Asp Glu Glu Glu
53 65 70 75
55 gcc gcg cgc aag gcc gga cac acc gtc aag tcc gcc cgc gag acc gcc 352
56 Ala Ala Arg Lys Ala Gly His Thr Val Lys Ser Ala Arg Glu Thr Ala
57 80 85 90
59 cag cac gcc gcc tcc gag acg ggg agg cag gcg agc ggc aag gtg ggg 400
60 Gln His Ala Ala Ser Glu Thr Gly Arg Gln Ala Ser Gly Lys Val Gly

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61	95	100	105	
63	gac gcc aag gag gcc gcg gag cag gcg gcg acc ggg gcg gcc aac aag	448		
64	Asp Ala Lys Glu Ala Ala Glu Gln Ala Ala Thr Gly Ala Ala Asn Lys			
65	110	115	120	
67	gcg ggg cag gcc aaa gac aag gcg gcg gag acg gtg aag ggc acg gcc	496		
68	Ala Gly Gln Ala Lys Asp Lys Ala Ala Glu Thr Val Lys Gly Thr Ala			
69	125	130	135	140
71	ggc gag gcg tcc aag aag gcg gag cag gcc aag cac aag acc aag gag	544		
72	Gly Glu Ala Ser Lys Lys Ala Glu Gln Ala Lys His Lys Thr Lys Glu			
73	145	150	155	
75	gcc gcg gag gcg gcc gcc aag acg ggc gcc gag acg cac gag cgg tcg	592		
76	Ala Ala Glu Ala Ala Ala Lys Thr Gly Ala Glu Thr His Glu Arg Ser			
77	160	165	170	
79	aag cag ggc aag gcc aag gtg gag gag atg gcc agg gag tgg tac gag	640		
80	Lys Gln Gly Lys Ala Lys Val Glu Glu Met Ala Arg Glu Trp Tyr Glu			
81	175	180	185	
83	aga gcc aag cac acg gcc ggg gag ggg tac gag acg ctg aag caa acc	688		
84	Arg Ala Lys His Thr Ala Gly Glu Gly Tyr Glu Thr Leu Lys Gln Thr			
85	190	195	200	
87	aag gac gcg gct gcg gag aag gca gcg gca gcc aag gac gcc gcc acg	736		
88	Lys Asp Ala Ala Ala Glu Lys Ala Ala Ala Ala Lys Asp Ala Ala Thr			
89	205	210	215	220
91	aac aag gcc ggt gcc gcc acg cag acg gcc gcg gag aag gca gcg gca	784		
92	Asn Lys Ala Gly Ala Ala Thr Gln Thr Ala Ala Glu Lys Ala Ala Ala			
93	225	230	235	
95	gcc aag gac acc gcc gcc ggt aag gcc aag gct gcg aag gac gct gcg	832		
96	Ala Lys Asp Thr Ala Ala Gly Lys Ala Lys Ala Ala Lys Asp Ala Ala			
97	240	245	250	
99	tgg gag gag aca ggc tct gcc aag gac gcc aca tgg cag gcg cag gag	880		
100	Trp Glu Glu Thr Gly Ser Ala Lys Asp Ala Thr Trp Gln Ala Gln Glu			
101	255	260	265	
103	aag ctg aag caa tac aac gac gcc gct tcg gag aag gcc gcg gca gcc	928		
104	Lys Leu Lys Gln Tyr Asn Asp Ala Ala Ser Glu Lys Ala Ala Ala Ala			
105	270	275	280	
107	aag gac gcc gac gct gag aag gcc gcg gca gcc aag gac gcg gcg tgg	976		
108	Lys Asp Ala Asp Ala Glu Lys Ala Ala Ala Ala Lys Asp Ala Ala Trp			
109	285	290	295	300
111	aag aac gcc gag gcg gcc aag gga acg gtc gga gag aag gca ggg gcg	1024		
112	Lys Asn Ala Glu Ala Ala Lys Gly Thr Val Gly Glu Lys Ala Gly Ala			
113	305	310	315	
115	gcc aag gac gcc acg ttg gag aag acc gag tcc gcg aag gac gcc gct	1072		
116	Ala Lys Asp Ala Thr Leu Glu Lys Thr Glu Ser Ala Lys Asp Ala Ala			
117	320	325	330	
119	tgg gag acg gcg gag gcg gcc aag ggc aag gct aac gag ggg tac gag	1120		
120	Trp Glu Thr Ala Glu Ala Ala Lys Gly Lys Ala Asn Glu Gly Tyr Glu			
121	335	340	345	
123	aag gtg aag gag aag gac gcg acc aag gaa aag ctc ggc gag gtg aag	1168		
124	Lys Val Lys Glu Lys Asp Ala Thr Lys Glu Lys Leu Gly Glu Val Lys			
125	350	355	360	

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W--> 127 gac aag gtc acc ggc gca gca tcc gac ggc aag gcg aag aag cnc cgc      1216
128 Asp Lys Val Thr Gly Ala Ala Ser Asp Gly Lys Ala Lys Lys Xaa Arg
129 365                               370                               375                               380
131 aat ggc gac gag ctg tgaatgaaca cgatccatcc gcatttcttg ccatagtccc      1271
132 Asn Gly Asp Glu Leu
133                               385
135 ttctttccatg aatgtttttca gtgttcttcg agctagtttt ttttatgttg ttccttttgt      1331
137 acaataacgt gtcccatatg tattgaacca tgcacgatca aacaagtttc tttctataaa      1391
139 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1420
142 <210> SEQ ID NO: 2
143 <211> LENGTH: 385
144 <212> TYPE: PRT
145 <213> ORGANISM: Bromus
147 <220> FEATURE:
148 <221> NAME/KEY: misc_feature
149 <222> LOCATION: (379)..(379)
150 <223> OTHER INFORMATION: The 'Xaa' at location 379 stands for His, Arg, Pro, or Leu.
152 <400> SEQUENCE: 2
154 Met Ala Val Met Ser Arg Ser Arg Arg Leu Ala Ala Pro Ala Leu Leu
155 1                               5                               10                               15
158 Val Leu Leu Ala Leu Ala Ala Val Ala Val Ala Glu Thr Thr Leu Asp
159                               20                               25                               30
162 Gly Ala Glu Val Ala Pro Gly Lys Glu Glu Ser Ser Trp Ala Gly Trp
163                               35                               40                               45
166 Ala Lys Asp Lys Val Ser Glu Gly Leu Gly Leu Asp Lys Ile Ser Glu
167                               50                               55                               60
170 Gly Leu Gly Leu Lys His His Ala Asp Glu Glu Glu Ala Ala Arg Lys
171 65                               70                               75                               80
174 Ala Gly His Thr Val Lys Ser Ala Arg Glu Thr Ala Gln His Ala Ala
175                               85                               90                               95
178 Ser Glu Thr Gly Arg Gln Ala Ser Gly Lys Val Gly Asp Ala Lys Glu
179                               100                              105                              110
182 Ala Ala Glu Gln Ala Ala Thr Gly Ala Ala Asn Lys Ala Gly Gln Ala
183                               115                              120                              125
186 Lys Asp Lys Ala Ala Glu Thr Val Lys Gly Thr Ala Gly Glu Ala Ser
187                               130                              135                              140
190 Lys Lys Ala Glu Gln Ala Lys His Lys Thr Lys Glu Ala Ala Glu Ala
191 145                              150                              155                              160
194 Ala Ala Lys Thr Gly Ala Glu Thr His Glu Arg Ser Lys Gln Gly Lys
195                               165                               170                               175
198 Ala Lys Val Glu Glu Met Ala Arg Glu Trp Tyr Glu Arg Ala Lys His
199                               180                              185                              190
202 Thr Ala Gly Glu Gly Tyr Glu Thr Leu Lys Gln Thr Lys Asp Ala Ala
203                               195                              200                              205
206 Ala Glu Lys Ala Ala Ala Ala Lys Asp Ala Ala Thr Asn Lys Ala Gly
207                               210                              215                              220
210 Ala Ala Thr Gln Thr Ala Ala Glu Lys Ala Ala Ala Lys Asp Thr
211 225                              230                              235                              240
214 Ala Ala Gly Lys Ala Lys Ala Ala Lys Asp Ala Ala Trp Glu Glu Thr

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215          245          250          255
218 Gly Ser Ala Lys Asp Ala Thr Trp Gln Ala Gln Glu Lys Leu Lys Gln
219          260          265          270
222 Tyr Asn Asp Ala Ala Ser Glu Lys Ala Ala Ala Lys Asp Ala Asp
223          275          280          285
226 Ala Glu Lys Ala Ala Ala Ala Lys Asp Ala Ala Trp Lys Asn Ala Glu
227          290          295          300
230 Ala Ala Lys Gly Thr Val Gly Glu Lys Ala Gly Ala Ala Lys Asp Ala
231 305          310          315          320
234 Thr Leu Glu Lys Thr Glu Ser Ala Lys Asp Ala Ala Trp Glu Thr Ala
235          325          330          335
238 Glu Ala Ala Lys Gly Lys Ala Asn Glu Gly Tyr Glu Lys Val Lys Glu
239          340          345          350
242 Lys Asp Ala Thr Lys Glu Lys Leu Gly Glu Val Lys Asp Lys Val Thr
243          355          360          365
W--> 246 Gly Ala Ala Ser Asp Gly Lys Ala Lys Lys Xaa Arg Asn Gly Asp Glu
247          370          375          380
250 Leu
251 385
254 <210> SEQ ID NO: 3
255 <211> LENGTH: 15
256 <212> TYPE: PRT
257 <213> ORGANISM: Bromus
259 <400> SEQUENCE: 3
261 Glu Thr Thr Leu Asp Gly Ala Glu Val Ala Pro Gly Lys Glu Glu
262 1          5          10          15
265 <210> SEQ ID NO: 4
266 <211> LENGTH: 6
267 <212> TYPE: PRT
268 <213> ORGANISM: Bromus
270 <400> SEQUENCE: 4
272 Lys Ala Ala Ala Ala Lys
273 1          5

```

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1212
Seq#:1; Xaa Pos. 379
Seq#:2; Xaa Pos. 379

VERIFICATION SUMMARY

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Input Set : A:\47968-A Sequence Listing.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30
L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1168
M:341 Repeated in SeqNo=1
L:246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:368